

OM protein - protein search, using sw model

Run on: September 28, 2001, 12:26:05 ; Search time 53.45 Seconds  
(without alignments)  
6,409 Million cell updates/sec

Title: US-09-551-645-1  
Perfect score: 49  
Sequence: 1 TFIGA1ATD1 10

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Database: SwissProt\_39

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	1645	1	OMP.B_RICTY
2	48	98.0	1643	1	OMP.B_RICPR
3	39	79.6	1300	1	120K_RICRI
4	39	79.6	1654	1	OMP.B_RICRI
5	36	73.5	174	1	CHCB_BOOMO
6	35	71.4	1254	1	YNCA_CAEEL
7	35	71.4	1656	1	OMP.B_RICJA
8	33	67.3	106	1	YCDZ_SALTY
9	33	67.3	179	1	THM1_ARATH
10	33	67.3	179	1	YCDZ_ECOLI
11	33	67.3	292	1	DHBD_ASPNG
12	33	67.3	531	1	C7E1_SORBI
13	33	67.3	553	1	HIS5_EMERI
14	32	65.3	167	1	CHCC_ANTPO
15	32	65.3	317	1	MSHR_BOVIN
16	32	65.3	317	1	MSHR_BOVIN
17	32	65.3	317	1	MSHR_CANFA
18	32	65.3	317	1	MSHR_CANFA
19	32	65.3	317	1	MSHR_CAPI
20	32	65.3	317	1	MSHR_CEREL
21	32	65.3	317	1	MSHR_DANDA
22	32	65.3	317	1	MSHR_HUMAN
23	32	65.3	317	1	MSHR_OVIMO
24	32	65.3	317	1	MSHR_RANTA
25	32	65.3	317	1	MSHR_SHEEP
26	32	65.3	317	1	MSHR_VILVU
27	32	65.3	317	1	MSHR_VILVU
28	31	63.3	540	1	MSHR_ECOLI
29	31	63.3	362	1	MSHR_ALCAA
30	31	63.3	392	1	YD33_MYCLE
31	31	63.3	392	1	CMR_SPRLI
32	31	63.3	427	1	Y686_CHLTR
33	31	63.3	716	1	VR8_MTV
					RP2153 dhori virus

# ALIGNMENTS

RESULT 1	OMP.B_RICTY	STANDARD	PRT: 1645 AA.
AC	P96989		
DT	15-JUL-1998 (Rel. 36, Created)		
DT	15-JUL-1998 (Rel. 36, Last sequence update)		
DT	01-OCT-2000 (Rel. 40, Last annotation update)		
DE	OUTER MEMBRANE PROTEIN B PRECURSOR (168 KDA SURFACE-LAYER PROTEIN)		
DE	(SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCA5) (Romp B)		
DE	(CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGEN)		
DE	(120 KDA OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA PEPTIDE]		
GN	SLP.		
OS	Rickettsia typhi.		
OC	Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;		
OC	Rickettsiaceae; Rickettsiae; Rickettsia.		
OX	NCBI_TaxID=785;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RE	STRAIN-WILMINGTON.		
RX	MEDLINE=94040787; PubMed=8224886;		
RA	Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;		
RT	*Cloning and sequence analysis of the gene encoding the crystalline		
RT	surface layer protein of Rickettsia typhi.*		
RL	Gene 133:129-133(1993)		
RM	[2]		
RP	PARTIAL SEQUENCE.		
RC	STRAIN-WILMINGTON.		
RX	MEDLINE=92114896; PubMed=1370573;		
RA	Ching W.M., Carl M., Dasch G.A.;		
RT	*Mapping of monoclonal antibody binding sites on CNR fragments of		
RT	the S-layer protein antigens of Rickettsia typhi and Rickettsia		
RT	proWazekii.*		
RL	Mol. Immunol. 29:95-105(1992).		
RN	[3]		
RP	IDENTIFICATION OF CLEAVAGE SITE.		
RX	MEDLINE=92104668; PubMed=1729180;		
RA	Hackstadt T., Messer R., Cleplak W., Peacock M.G.;		
RT	*Evidence for proteolytic cleavage of the 120-kilodalton outer		
RT	membrane protein of rickettsiae: Identification of an avirulent		
RT	mutant deficient in processing.*		
RL	Infect. Immun. 60:159-165(1992).		
CC	- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR		
CC	STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL		
CC	VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.		
CC	- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.		
CC	SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A		
CC	S-LAYER WITH HEXAGONAL SYMMETRY.		
CC			
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Seq ID NO: 1

DR EMBL: L04661; AAB48987.1; -  
 KW Antigen: S-layer; Transmembrane; Cell wall.  
 FT CHAIN 1 1353 120 KDA SURFACE-EXPOSED PROTEIN.  
 FT TRANSMEM 1415 1645 32 KDA BETA PEPTIDE.  
 FT TRANSMEM 1415 1429 MEMBRANE ANCHOR (POTENTIAL).  
 FT CONFLICT 657 657 H -> N (IN REF. 2).  
 FT CONFLICT 842 842 V -> I (IN REF. 2).  
 FT CONFLICT 1071 1071 G -> A (IN REF. 2).  
 FT CONFLICT 1306 1306 G -> S (IN REF. 2).  
 FT SEQUENCE 1645 AA; 169698 MW; 0CB5641C7ED185EE CRC64;

Query Match 100.0%; Score 49; DB 1; Length 1645;  
 Best Local Similarity 100.0%; Pred. No. 0.048;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TFGAIADT 10  
 DB 1296 TFGAIADT 1305

## RESULT 2

OMP\_RICPR STANDARD; PRT; 1643 AA.  
 AC 053020; Q9ZCM0;  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE OUTER MEMBRANE PROTEIN B PRECURSOR (168 KDA SURFACE-LAYER PROTEIN)  
 DE (SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCA5) (ROMP B)  
 DE (CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGEN)  
 DE (120 KDA OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA PEPTIDE).  
 OS OMPB OR SPAP OR SPA OR RP704  
 OS Rickettsia prowazekii.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
 OC Rickettsiaceae; Rickettsiinae; Rickettsia.  
 NC NCBI\_TaxID=782;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC STRAIN-BREINL.  
 RA MEDLINE-91045972; PubMed-2122457;  
 RA Carl M., Dobson M.E., Ching W.M., Dasch G.A.;  
 RT "Characterization of the gene encoding the protective paracrystalline-  
 RT surface-layer protein of Rickettsia prowazekii: presence of a  
 RT truncated identical homolog in Rickettsia typhi."  
 RT Proc. Natl. Acad. Sci. U.S.A. 87:8237-8241(1990).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BREINL.  
 RA Moron C.G., Yu X.J., Walker D.H.;  
 RT "Sequence analysis of ompb of Rickettsia prowazekii."  
 RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 RL [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MADRID E;  
 RA MEDLINE-99039499; PubMed-9823893;  
 RA Andersson S.G.E., Zomrodipour A., Andersson J.O.,  
 RA Slicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,  
 RA Eriksson A.-S., Winkler H.H., Kurland C.G.;  
 RT "The genome sequence of Rickettsia prowazekii and the origin of  
 RT mitochondria."  
 RT Nature 396:133-140(1998).  
 RL [4]  
 RP PARTIAL SEQUENCE.  
 RC STRAIN-BREINL.  
 RA MEDLINE-92114896; PubMed-1370573;  
 RA Ching W.M., Carl M., Dasch G.A.;  
 RT "Mapping of monoclonal antibody binding sites on CNB: fragments of  
 RT the S-layer protein antigens of Rickettsia typhi and Rickettsia  
 RT prowazekii."  
 RT Mol. Immunol. 29:95-105(1992).  
 RL [5]

RX MEDLINE-92104668; PubMed-1729180;  
 RA Hackstadt T., Messer R., Cleplak W. Jr., Peacock M.G.;  
 RT "Evidence for proteolytic cleavage of the 120-kilodalton outer  
 RT membrane protein of rickettsiae: identification of an avirulent mutant  
 RT deficient in processing."  
 RL Infect. Immun. 60:159-165(1992).  
 CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR  
 CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL  
 CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.  
 CC -1- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.  
 CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-  
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 CC  
 DR EMBL: M37647; AAA26390.1; ALT\_INIT.  
 DR EMBL: A161079; AAD42234.1;  
 DR EMBL: A1235273; CAAL5140.1;  
 KW Antigen: S-layer; Cell wall.  
 FT CHAIN 1 1328 120 KDA SURFACE-EXPOSED PROTEIN.  
 FT VARIANT 1329 1643 32 KDA BETA PEPTIDE.  
 FT VARIANT 1329 1643 V -> A (IN STRAIN BREINL).  
 FT VARIANT 1010 1010 Y -> D (IN STRAIN BREINL).  
 FT VARIANT 1490 1450 A -> S (IN STRAIN BREINL).  
 FT CONFLICT 178 179 AA -> VC (IN REF. 1).  
 FT CONFLICT 191 201 T -> I (IN REF. 1).  
 FT CONFLICT 212 212 T -> L (IN REF. 1).  
 FT CONFLICT 313 313 D -> G (IN REF. 2).  
 FT CONFLICT 1104 1104 T -> S (IN REF. 2).  
 FT CONFLICT 1123 1123  
 FT SEQUENCE 1643 AA; 169854 MW; 735FDF32E346CC CRC64;

Query Match 98.0%; Score 48; DB 1; Length 1643;  
 Best Local Similarity 90.0%; Pred. No. 0.077;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TFGAIADT 10  
 DB 1296 TFGAIADT 1305

RESULT 3  
 ID 120K\_RICRI STANDARD; PRT; 1300 AA.  
 AC P14914;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE 120 KDA SURFACE-EXPOSED PROTEIN.  
 GN P120.  
 OS Rickettsia rickettsii.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
 OC Rickettsiaceae; Rickettsiinae; Rickettsia.  
 NC NCBI\_TaxID=783;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-R.  
 RA MEDLINE-90136087; PubMed-2515418;  
 RA Gilmore R.D. Jr., Joste N., McDonald G.A.;  
 RT "Cloning, expression and sequence analysis of the gene encoding the  
 RT 120 kD surface-exposed protein of Rickettsia rickettsii."  
 RL Mol. Microbiol. 3:1579-1586(1989).  
 CC -1- FUNCTION: MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS  
 CC RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.  
 CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-